



SEQUENCE LISTING

<110> Madison, Edgar
Ong, Edgar
Yeh, Juinn-Chern

<120> NUCLEIC ACID MOLECULES ENCODING SERINE PROTEASE 16, THE
ENCODED PROTEINS AND METHODS BASED THEREON

<130> 24745-1625

<140> 10/612,466

<141> 2003-07-01

<150> 60/394,347

<151> 2002-07-02

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<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (23)...(2589)

<223> Nucleotide sequence encoding MTSP1

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<308> GenBank #AR081724

<309> 2000-08-31

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Gly Gly Pro Lys Asp Phe Gly Ala Gly Leu Lys Tyr Asn Ser Arg His	
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gag aaa gtg aat ggc ttg gag gaa ggc gtg gag ttc ctg cca gtc aac	148
Glu Lys Val Asn Gly Leu Glu Glu Gly Val Glu Phe Leu Pro Val Asn	
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aac gtc aag aag gtg gaa aag cat ggc ccg ggg cgc tgg gtg gtg ctg	196
Asn Val Lys Lys Val Glu Lys His Gly Pro Gly Arg Trp Val Val Leu	
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gca gcc gtg ctg atc ggc ctc ctc ttg gtc ttg ctg ggg atc ggc ttc	244
Ala Ala Val Leu Ile Gly Leu Leu Leu Val Leu Leu Gly Ile Gly Phe	
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Leu Val Trp His Leu Gln Tyr Arg Asp Val Arg Val Gln Lys Val Phe	
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Asn	Ser	Asn	Ser	Thr	Glu	Phe	Val	Ser	Leu	Ala	Ser	Lys	Val	Lys	Asp		
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gcg	ctg	aag	ctg	ctg	tac	agc	gga	gtc	cca	ttc	ctg	ggc	ccc	tac	cac	436	
Ala	Leu	Lys	Leu	Leu	Tyr	Ser	Gly	Val	Pro	Phe	Leu	Gly	Pro	Tyr	His		
		125					130					135					
aag	gag	tcg	gct	gtg	acg	gcc	ttc	agc	gag	ggc	agc	gtc	atc	gcc	tac	484	
Lys	Glu	Ser	Ala	Val	Thr	Ala	Phe	Ser	Glu	Gly	Ser	Val	Ile	Ala	Tyr		
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tac	tgg	tct	gag	ttc	agc	atc	ccg	cag	cac	ctg	gtg	gag	gag	gcc	gag	532	
Tyr	Trp	Ser	Glu	Phe	Ser	Ile	Pro	Gln	His	Leu	Val	Glu	Glu	Ala	Glu		
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Ser	Leu	Lys	Ser	Phe	Val	Val	Thr	Ser	Val	Val	Ala	Phe	Pro	Thr	Asp		
			190					195					200				
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Ser	Lys	Thr	Val	Gln	Arg	Thr	Gln	Asp	Asn	Ser	Cys	Ser	Phe	Gly	Leu		
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His	Ala	Arg	Gly	Val	Glu	Leu	Met	Arg	Phe	Thr	Thr	Pro	Gly	Phe	Pro		
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Asp	Ser	Pro	Tyr	Pro	Ala	His	Ala	Arg	Cys	Gln	Trp	Ala	Leu	Arg	Gly		
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Ser	Pro	Met	Glu	Pro	His	Ala	Leu	Val	Gln	Leu	Cys	Gly	Thr	Tyr	Pro		
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ccc	tcc	tac	aac	ctg	acc	ttc	cac	tcc	tcc	cag	aac	gtc	ctg	ctc	atc	964	
Pro	Ser	Tyr	Asn	Leu	Thr	Phe	His	Ser	Ser	Gln	Asn	Val	Leu	Leu	Ile		
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aca	ctg	ata	acc	aac	act	gag	cgg	cgg	cat	ccc	ggc	ttt	gag	gcc	acc	1012	
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Phe	Phe	Gln	Leu	Pro	Arg	Met	Ser	Ser	Cys	Gly	Gly	Arg	Leu	Arg	Lys		

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Lys	Val	Ser	Phe	Lys	Phe	Phe	Tyr	Leu	Leu	Glu	Pro	Gly	Val	Pro	Ala			
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ggc	acc	tgc	ccc	aag	gac	tac	gtg	gag	atc	aat	ggg	gag	aaa	tac	tgc	1252		
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Asp Cys Gly Leu Arg Ser Phe Thr Arg Gln Ala Arg Val Val Gly Gly	
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Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val Ser Leu His Ala	
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Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr	
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Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu His Asp Gln Ser	
670 675 680	
cag cgc agc gcc cct ggg gtg cag gag cgc agg ctc aag cgc atc atc	2116
Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu Lys Arg Ile Ile	
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Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu	
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ctg gag ctg gag aaa ccg gca gag tac agc tcc atg gtg cgg ccc atc	2212
Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met Val Arg Pro Ile	
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tgc ctg ccg gac gcc tcc cat gtc ttc cct gcc ggc aag gcc atc tgg	2260
Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly Lys Ala Ile Trp	
735 740 745	
gtc acg ggc tgg gga cac acc cag tat gga ggc act ggc gcg ctg atc	2308
Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile	
750 755 760	
ctg caa aag ggt gag atc cgc gtc atc aac cag acc acc tgc gag aac	2356
Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr Thr Cys Glu Asn	
765 770 775	
ctc ctg ccg cag cag atc acg ccg cgc atg atg tgc gtg ggc ttc ctc	2404
Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys Val Gly Phe Leu	
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agc ggc ggc gtg gac tcc tgc cag ggt gat tcc ggg gga ccc ctg tcc	2452
Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser	
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Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly Val Val Ser Trp	
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Gly	Ala	Gly	Leu 20	Lys	Tyr	Asn	Ser	Arg 25	His	Glu	Lys	Val	Asn 30	Gly	Leu
Glu	Glu	Gly 35	Val	Glu	Phe	Leu	Pro 40	Val	Asn	Asn	Val	Lys 45	Lys	Val	Glu
Lys	His 50	Gly	Pro	Gly	Arg	Trp 55	Val	Val	Leu	Ala	Ala 60	Val	Leu	Ile	Gly
Leu 65	Leu	Leu	Val	Leu	Leu 70	Gly	Ile	Gly	Phe	Leu 75	Val	Trp	His	Leu	Gln 80
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Thr 210	Gln	Asp	Asn	Ser	Cys	Ser 215	Phe	Gly	Leu	His	Ala 220	Arg	Gly	Val	Glu
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Val	Val	Thr	Ser	Asn	Ser	Asn	Lys	Ile	Thr	Val	Arg	Phe	His	Ser	Asp
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Gln	Ser	Tyr	Thr	Asp	Thr	Gly	Phe	Leu	Ala	Glu	Tyr	Leu	Ser	Tyr	Asp
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	690					695					700				
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Ala	Glu	Tyr	Ser	Ser	Met	Val	Arg	Pro	Ile	Cys	Leu	Pro	Asp	Ala	Ser
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His	Val	Phe	Pro	Ala	Gly	Lys	Ala	Ile	Trp	Val	Thr	Gly	Trp	Gly	His
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Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly				800
	805		810	815
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<211> 3147

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (1865)...(2590)

<223> Nucleic acid sequence of protease domain of MTSP1

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tcgt gtt gtt ggg ggc acg gat gcg	gat gag ggc gag tgg ccc tgg cag					1909
Val Val Gly Gly Thr Asp Ala	Asp Glu Gly Glu Trp Pro Trp Gln					
1	5	10	15			

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Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp	
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Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly	
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Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg	
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Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp	
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tat gac atc gcg ctg ctg gag ctg gag aaa ccg gca gag tac agc tcc	2197
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Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala	
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Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser	
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Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly	
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Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr	
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Gly Val *	
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Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
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Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
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His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
 65      70      75
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
 85      90      95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
100      105      110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
115      120      125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
130      135      140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145      150      155
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
165      170      175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
180      185      190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
195      200      205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
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Val

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<220>
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Ile Pro Gly Ala Phe Gln Asp Ser Ala Leu Ser Pro Thr Gln Glu Glu	
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cct gaa gat ctg gac tgc ggg cgc cct gag ccc tcg gcc cgc atc gtg	144
Pro Glu Asp Leu Asp Cys Gly Arg Pro Glu Pro Ser Ala Arg Ile Val	
35 40 45	
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Gly Gly Ser Asn Ala Gln Pro Gly Thr Trp Pro Trp Gln Val Ser Leu	
50 55 60	
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His His Gly Gly Gly His Ile Cys Gly Gly Ser Leu Ile Ala Pro Ser	
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Trp Val Leu Ser Ala Ala His Cys Phe Met Thr Asn Gly Thr Leu Glu	
85 90 95	
ccc gcg gcc gag tgg tcg gta ctg ctg ggc gtg cac tcc cag gac ggg	336
Pro Ala Ala Glu Trp Ser Val Leu Leu Gly Val His Ser Gln Asp Gly	
100 105 110	
ccc ctg gac ggc gcg cac acc cgc gca gtg gcc gcc atc gtg gtg ccg	384
Pro Leu Asp Gly Ala His Thr Arg Ala Val Ala Ala Ile Val Val Pro	
115 120 125	
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Ala Asn Tyr Ser Gln Val Glu Leu Gly Ala Asp Leu Ala Leu Leu Arg	
130 135 140	
ctg gcc tca ccc gcc agc ctg ggc ccc gcc gtg tgg cct gtc tgc ctg	480
Leu Ala Ser Pro Ala Ser Leu Gly Pro Ala Val Trp Pro Val Cys Leu	
145 150 155 160	
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Pro Arg Ala Ser His Arg Phe Val His Gly Thr Ala Cys Trp Ala Thr	
165 170 175	
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Gly Trp Gly Asp Val Gln Glu Ala Asp Pro Leu Pro Leu Pro Trp Val	
180 185 190	
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Leu Gln Glu Val Glu Leu Arg Leu Leu Gly Glu Ala Thr Cys Gln Cys	
195 200 205	
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Gly Met Leu Cys Ala Gly Tyr Pro Gly Gly Arg Arg Asp Thr Cys Gln	
225 230 235 240	
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Gly Asp Ser Gly Gly Pro Leu Val Cys Glu Glu Gly Gly Arg Trp Phe	
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Gln	Ala	Gly	Ile	Thr	Ser	Phe	Gly	Phe	Gly	Cys	Gly	Arg	Arg	Asn	Arg		
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Pro	Gly	Val	Phe	Thr	Ala	Val	Ala	Thr	Tyr	Glu	Ala	Trp	Ile	Arg	Glu		
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cag	gtg	atg	ggg	tca	gag	cct	ggg	cct	gcc	ttt	ccc	acc	cag	ccc	cag	912	
Gln	Val	Met	Gly	Ser	Glu	Pro	Gly	Pro	Ala	Phe	Pro	Thr	Gln	Pro	Gln		
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aag	acc	cag	tca	gat	ccc	cag	gag	ccc	agg	gag	gag	aac	tgc	acc	att	960	
Lys	Thr	Gln	Ser	Asp	Pro	Gln	Glu	Pro	Arg	Glu	Glu	Asn	Cys	Thr	Ile		
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Ala	Leu	Pro	Glu	Cys	Gly	Lys	Ala	Pro	Arg	Pro	Gly	Ala	Trp	Pro	Trp		
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Glu	Ala	Gln	Val	Met	Val	Pro	Gly	Ser	Arg	Pro	Cys	His	Gly	Ala	Leu		
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Val	Ser	Glu	Ser	Trp	Val	Leu	Ala	Pro	Ala	Ser	Cys	Phe	Leu	Asp	Pro		
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aac	agc	tcc	gac	agc	cca	ccc	cgc	gac	ctc	gac	gcc	tgg	cgc	gtg	ctg	1152	
Asn	Ser	Ser	Asp	Ser	Pro	Pro	Arg	Asp	Leu	Asp	Ala	Trp	Arg	Val	Leu		
		370					375				380						
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Leu	Pro	Ser	His	Pro	Arg	Ala	Glu	Arg	Val	Ala	Arg	Leu	Val	Gln	His		
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gag	aac	gct	tgc	tgg	gac	aac	gcc	ccg	gac	ctg	gcg	ctg	ctg	cag	ctg	1248	
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Arg	Thr	Pro	Val	Asn	Leu	Ser	Ala	Ala	Ser	Arg	Pro	Val	Cys	Leu	Pro		
			420					425					430				
cac	ccg	gaa	cac	tac	ttc	ctg	ccc	ggg	agc	cgc	tgc	cgc	ctg	gcc	cgc	1344	
His	Pro	Glu	His	Tyr	Phe	Leu	Pro	Gly	Ser	Arg	Cys	Arg	Leu	Ala	Arg		
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Trp	Gly	Arg	Gly	Glu	Pro	Ala	Leu	Gly	Pro	Gly	Ala	Leu	Leu	Glu	Ala		
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gag	ctg	tta	ggc	ggc	tgg	tgg	tgc	cac	tgc	ctg	tac	ggc	cgc	cag	ggg	1440	
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gcg	gca	gta	ccg	ctg	ccc	gga	gac	ccg	ccg	cac	gcg	ctc	tgc	cct	gcc	1488	
Ala	Ala	Val	Pro	Leu	Pro	Gly	Asp	Pro	Pro	His	Ala	Leu	Cys	Pro	Ala		
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tac	cag	gaa	aag	gag	gag	gtg	ggc	agc	tgc	tgg	aat	gac	tgc	cgt	tgg	1536	
Tyr	Gln	Glu	Lys	Glu	Glu	Val	Gly	Ser	Cys	Trp	Asn	Asp	Ser	Arg	Trp		

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Ser	Leu	Leu	Cys	Gln	Glu	Glu	Gly	Thr	Trp	Phe	Leu	Ala	Gly	Ile	Arg	
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Asp	Phe	Pro	Ser	Gly	Cys	Leu	Arg	Pro	Arg	Ala	Phe	Phe	Pro	Leu	Gln	
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Asp	Gln	Leu	Ala	Trp	Asp	Trp	Gly	Pro	Asp	Gly	Glu	Glu	Thr	Glu	Thr	
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Gln	Thr	Cys	Pro	Pro	His	Thr	Glu	His	Gly	Ala	Cys	Gly	Leu	Arg	Leu	
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gag	gct	gct	cca	gtg	ggg	gtc	ctg	tgg	ccc	tgg	ctg	gca	gag	gtg	cat	1824
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Val	Ala	Gly	Asp	Arg	Val	Cys	Thr	Gly	Ile	Leu	Leu	Ala	Pro	Gly	Trp	
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Val	Leu	Ala	Ala	Thr	His	Cys	Val	Leu	Arg	Pro	Gly	Ser	Thr	Thr	Val	
	625					630				635					640	
cct	tac	att	gaa	gtg	tat	ctg	ggc	cgg	gca	ggg	gcc	agc	tcc	ctc	cca	1968
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Gln	Gly	His	Gln	Met	Thr	Ser	Ala	Pro	Pro	Leu	Leu	Cys	Gln	Met	Thr	
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Pro	His	Ala	Val	Tyr	Phe	Leu	Leu	Leu	Leu	Thr	Leu	Leu	Ile	Gln	Ser	
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2293

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Gly Gly Ser Asn Ala Gln Pro Gly Thr Trp Pro Trp Gln Val Ser Leu
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His His Gly Gly Gly His Ile Cys Gly Gly Ser Leu Ile Ala Pro Ser
65 70 75 80
Trp Val Leu Ser Ala Ala His Cys Phe Met Thr Asn Gly Thr Leu Glu
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Pro Ala Ala Glu Trp Ser Val Leu Leu Gly Val His Ser Gln Asp Gly
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Pro Leu Asp Gly Ala His Thr Arg Ala Val Ala Ala Ile Val Val Pro
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Ala Asn Tyr Ser Gln Val Glu Leu Gly Ala Asp Leu Ala Leu Leu Arg
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Leu Ala Ser Pro Ala Ser Leu Gly Pro Ala Val Trp Pro Val Cys Leu
145 150 155 160
Pro Arg Ala Ser His Arg Phe Val His Gly Thr Ala Cys Trp Ala Thr
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Gly Trp Gly Asp Val Gln Glu Ala Asp Pro Leu Pro Leu Pro Trp Val
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Leu Gln Glu Val Glu Leu Arg Leu Leu Gly Glu Ala Thr Cys Gln Cys
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Leu Tyr Ser Gln Pro Gly Pro Phe Asn Leu Thr Leu Gln Ile Leu Pro
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Gly Met Leu Cys Ala Gly Tyr Pro Gly Gly Arg Arg Asp Thr Cys Gln
225 230 235 240
Gly Asp Ser Gly Gly Pro Leu Val Cys Glu Glu Gly Gly Arg Trp Phe
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Gln Ala Gly Ile Thr Ser Phe Gly Phe Gly Cys Gly Arg Arg Asn Arg
260 265 270
Pro Gly Val Phe Thr Ala Val Ala Thr Tyr Glu Ala Trp Ile Arg Glu
275 280 285
Gln Val Met Gly Ser Glu Pro Gly Pro Ala Phe Pro Thr Gln Pro Gln
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Lys Thr Gln Ser Asp Pro Gln Glu Pro Arg Glu Glu Asn Cys Thr Ile
305 310 315 320
Ala Leu Pro Glu Cys Gly Lys Ala Pro Arg Pro Gly Ala Trp Pro Trp
325 330 335
Glu Ala Gln Val Met Val Pro Gly Ser Arg Pro Cys His Gly Ala Leu
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Val Ser Glu Ser Trp Val Leu Ala Pro Ala Ser Cys Phe Leu Asp Pro
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Glu	Asn	Ala	Ser	Trp	Asp	Asn	Ala	Pro	Asp	Leu	Ala	Leu	Leu	Gln	Leu
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Arg	Thr	Pro	Val	Asn	Leu	Ser	Ala	Ala	Ser	Arg	Pro	Val	Cys	Leu	Pro
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His	Pro	Glu	His	Tyr	Phe	Leu	Pro	Gly	Ser	Arg	Cys	Arg	Leu	Ala	Arg
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Trp	Gly	Arg	Gly	Glu	Pro	Ala	Leu	Gly	Pro	Gly	Ala	Leu	Leu	Glu	Ala
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Glu	Leu	Leu	Gly	Gly	Trp	Trp	Cys	His	Cys	Leu	Tyr	Gly	Arg	Gln	Gly
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Tyr	Gln	Glu	Lys	Glu	Glu	Val	Gly	Ser	Cys	Trp	Asn	Asp	Ser	Arg	Trp
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	515						520					525			
Asp	Phe	Pro	Ser	Gly	Cys	Leu	Arg	Pro	Arg	Ala	Phe	Phe	Pro	Leu	Gln
	530					535					540				
Thr	His	Gly	Pro	Trp	Ile	Ser	His	Val	Thr	Arg	Gly	Ala	Tyr	Leu	Glu
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Asp	Gln	Leu	Ala	Trp	Asp	Trp	Gly	Pro	Asp	Gly	Glu	Glu	Thr	Glu	Thr
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Gln	Thr	Cys	Pro	Pro	His	Thr	Glu	His	Gly	Ala	Cys	Gly	Leu	Arg	Leu
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	595						600					605			
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□